

#7

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/703,253

DATE: 08/15/2001

TIME: 08:20:17

Input Set : A:\lex81usa SEQLIST.TXT

Output Set: N:\CRF3\08132001\I703253.raw

ENTERED

ENTERED

4 <110> APPLICANT: Harras, Marie
 5 Donoho, Gregory
 6 Turner, C. Alexander Jr.
 7 Nehls, Michael
 8 Friedrich, Glenn
 9 Zambrowicz, Brian
 10 Sands, Arthur T.
 12 <120> TITLE OF INVENTION: Novel Human Transporter Proteins and
 13 Polynucleotides Encoding the Same
 16 <130> FILE REFERENCE: LEX-0081-USA
 18 <140> CURRENT APPLICATION NUMBER: US/09/703,253
 18 <141> CURRENT FILING DATE: 2000-10-31
 18 <150> PRIOR APPLICATION NUMBER: US 60/163,018
 19 <151> PRIOR FILING DATE: 1999-11-02
 21 <160> NUMBER OF SEQ ID NOS: 25
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1977
 27 <212> TYPE: DNA
 28 <213> ORGANISM: homo sapiens
 30 <400> SEQUENCE: 1

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32	cggtgtgacca	gtgaagttct	cacttgcat	aagctgatta	aaatgtacac	atgggagaaa	120
33	ccatttgcaa	aaatcattga	agacctaaga	aggaaggaaa	ggaagctatt	ggagaagtgc	180
34	gggcttgctc	agagcctgac	aagtataacc	ttgttcac	tccccacagt	ggccacagcg	240
35	gtctgggttc	tcatccacac	atccttaaag	ctgaaactca	cagcgtcaat	ggccttcagc	300
36	atgctggcct	ccttgaatct	ccttcggctg	tcagtgttct	ttgtgcctat	tgagtcacaa	360
37	ggtctcacga	attccaagtc	tgagtgatg	aggttcaaga	agtttttct	ccaggagagc	420
38	cctgttttct	atgtccagac	attacaagac	cccagcaaag	ctctggtctt	tgaggaggcc	480
39	accttgatc	ggcaacagac	ctgtcccggg	atcgtcaatg	gggcaactga	gctggagagg	540
40	aacgggcatg	cttctgaggg	gatgaccagg	cctagagatg	ccctcggggc	agaggaagaa	600
41	gggaacagcc	tgggccca	gttgacaa	atcaacctgg	tggtgtccaa	gggatgatg	660
42	ttaggggtct	gcggcaacac	ggggagtgg	aagagcagcc	tggtgtcagc	catcctggag	720
43	gagatgcact	tgctcgaggg	ctcggtgagg	gtgcaggaaa	gcctggccta	tgccccccag	780
44	caggcctgga	tcgtcagcgg	gaacatcagg	gagaacatcc	tcattggagg	cgcatatgac	840
45	aaggcccgat	acctccaggt	gctccactgc	tgctccctga	atcgggacct	ggaacttctg	900
46	ccctttggag	acatgacaga	gattggagag	cggggcctca	acctctctgg	ggggcagaaa	960
47	cagaggatca	gcctggcccc	cgccgtctat	tccgaccgtc	agatctacct	gctggacgac	1020
48	cccctgtctg	ctgtggacgc	ccacgtgggg	aagcacattt	ttgaggagtg	cattaagaag	1080
49	acactcaggg	ggaagacggt	cgtcctgggt	accaccagc	tgagtgactt	agaattttgt	1140
50	ggccagatca	ttttgttgga	aaatgggaaa	atctgtgaaa	atggaaactca	cagtgaagta	1200
51	atgcagaaaa	aggggaaata	tgcccaactt	atccagaaga	tgacaaagga	agccacttcg	1260
52	gacatgttgc	aggacacagc	aaagatagca	gagaagccaa	aggtagaaag	tcaggctctg	1320
53	gccacctccc	tggaagagtc	tctcaacgga	aatgctgtgc	cgagagcatca	gctcacacag	1380
54	gaggaggaga	tggaagaagg	ctccttgagt	tggagggtct	accaccacta	catccaggca	1440
55	gctggagggt	acatggtctc	ttgcataatt	ttcttcttcg	tggtgctgat	cgtcttctta	1500
56	acgatcttca	gcttctggtg	gctgagctac	tggttgaggc	agggctcggg	gaccaatagc	1560

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57 agccgagaga gcaatggaac catggcagac ctgggcaaca ttgcagacaa tcctcaactg 1620
58 tccttctacc agctggtgta cgggctcaac gccctgctcc tcactgtgtt gggggtctgc 1680
59 tcctcaggga ttttcaccaa ggtcacgagg aaggcatcca cggccctgca caacaagctc 1740
60 ttcaacaagg ttttcgctg ccccatgagt ttctttgaca ccatcccaat aggccggtt 1800
61 ttgaactgct tcgcaggga cttggaacag ctggaccagc tcttgcccat cttttcagag 1860
62 cagttcctgg tcctgtcctt aatggtgatc gccgtcctgt tgattgtcag tgtgctgtct 1920
63 ccatatatcc tgtaaatggg agccataatc atggttattt gcttcattta ttatatg 1977
64 <210> SEQ ID NO: 2
65 <211> LENGTH: 659
66 <212> TYPE: PRT
67 <213> ORGANISM: homo sapiens
68 <400> SEQUENCE: 2
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72 1 5 10 15
73 Asp Gln Arg Ile Arg Val Thr Ser Glu Val Leu Thr Cys Ile Lys Leu
74 20 25 30
75 Ile Lys Met Tyr Thr Trp Glu Lys Pro Phe Ala Lys Ile Ile Glu Asp
76 35 40 45
77 Leu Arg Arg Lys Glu Arg Lys Leu Leu Glu Lys Cys Gly Leu Val Gln
78 50 55 60
79 Ser Leu Thr Ser Ile Thr Leu Phe Ile Ile Pro Thr Val Ala Thr Ala
80 65 70 75 80
81 Val Trp Val Leu Ile His Thr Ser Leu Lys Leu Lys Leu Thr Ala Ser
82 85 90 95
83 Met Ala Phe Ser Met Leu Ala Ser Leu Asn Leu Leu Arg Leu Ser Val
84 100 105 110
85 Phe Phe Val Pro Ile Ala Val Lys Gly Leu Thr Asn Ser Lys Ser Ala
86 115 120 125
87 Val Met Arg Phe Lys Lys Phe Phe Leu Gln Glu Ser Pro Val Phe Tyr
88 130 135 140
89 Val Gln Thr Leu Gln Asp Pro Ser Lys Ala Leu Val Phe Glu Glu Ala
90 145 150 155 160
91 Thr Leu Ser Trp Gln Gln Thr Cys Pro Gly Ile Val Asn Gly Ala Leu
92 165 170 175
93 Glu Leu Glu Arg Asn Gly His Ala Ser Glu Gly Met Thr Arg Pro Arg
94 180 185 190
95 Asp Ala Leu Gly Pro Glu Glu Glu Gly Asn Ser Leu Gly Pro Glu Leu
96 195 200 205
97 His Lys Ile Asn Leu Val Val Ser Lys Gly Met Met Leu Gly Val Cys
98 210 215 220
99 Gly Asn Thr Gly Ser Gly Lys Ser Ser Leu Leu Ser Ala Ile Leu Glu
100 225 230 235 240
101 Glu Met His Leu Leu Glu Gly Ser Val Gly Val Gln Gly Ser Leu Ala
102 245 250 255
103 Tyr Val Pro Gln Gln Ala Trp Ile Val Ser Gly Asn Ile Arg Glu Asn
104 260 265 270
105 Ile Leu Met Gly Gly Ala Tyr Asp Lys Ala Arg Tyr Leu Gln Val Leu
106 275 280 285
107 His Cys Cys Ser Leu Asn Arg Asp Leu Glu Leu Leu Pro Phe Gly Asp

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108      290      295      300
109 Met Thr Glu Ile Gly Glu Arg Gly Leu Asn Leu Ser Gly Gly Gln Lys
110 305      310      315      320
111 Gln Arg Ile Ser Leu Ala Arg Ala Val Tyr Ser Asp Arg Gln Ile Tyr
112      325      330      335
113 Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ala His Val Gly Lys His
114      340      345      350
115 Ile Phe Glu Glu Cys Ile Lys Lys Thr Leu Arg Gly Lys Thr Val Val
116      355      360      365
117 Leu Val Thr His Gln Leu Gln Tyr Leu Glu Phe Cys Gly Gln Ile Ile
118      370      375      380
119 Leu Leu Glu Asn Gly Lys Ile Cys Glu Asn Gly Thr His Ser Glu Leu
120 385      390      395      400
121 Met Gln Lys Lys Gly Lys Tyr Ala Gln Leu Ile Gln Lys Met His Lys
122      405      410      415
123 Glu Ala Thr Ser Asp Met Leu Gln Asp Thr Ala Lys Ile Ala Glu Lys
124      420      425      430
125 Pro Lys Val Glu Ser Gln Ala Leu Ala Thr Ser Leu Glu Glu Ser Leu
126      435      440      445
127 Asn Gly Asn Ala Val Pro Glu His Gln Leu Thr Gln Glu Glu Glu Met
128      450      455      460
129 Glu Glu Gly Ser Leu Ser Trp Arg Val Tyr His His Tyr Ile Gln Ala
130 465      470      475      480
131 Ala Gly Gly Tyr Met Val Ser Cys Ile Ile Phe Phe Phe Val Val Leu
132      485      490      495
133 Ile Val Phe Leu Thr Ile Phe Ser Phe Trp Trp Leu Ser Tyr Trp Leu
134      500      505      510
135 Glu Gln Gly Ser Gly Thr Asn Ser Ser Arg Glu Ser Asn Gly Thr Met
136      515      520      525
137 Ala Asp Leu Gly Asn Ile Ala Asp Asn Pro Gln Leu Ser Phe Tyr Gln
138      530      535      540
139 Leu Val Tyr Gly Leu Asn Ala Leu Leu Leu Ile Cys Val Gly Val Cys
140 545      550      555      560
141 Ser Ser Gly Ile Phe Thr Lys Val Thr Arg Lys Ala Ser Thr Ala Leu
142      565      570      575
143 His Asn Lys Leu Phe Asn Lys Val Phe Arg Cys Pro Met Ser Phe Phe
144      580      585      590
145 Asp Thr Ile Pro Ile Gly Arg Leu Leu Asn Cys Phe Ala Gly Asp Leu
146      595      600      605
147 Glu Gln Leu Asp Gln Leu Leu Pro Ile Phe Ser Glu Gln Phe Leu Val
148      610      615      620
149 Leu Ser Leu Met Val Ile Ala Val Leu Leu Ile Val Ser Val Leu Ser
150 625      630      635      640
151 Pro Tyr Ile Leu Leu Met Gly Ala Ile Ile Met Val Ile Cys Phe Ile
152      645      650      655
153 Tyr Tyr Met
156 <210> SEQ ID NO: 3
157 <211> LENGTH: 2115
158 <212> TYPE: DNA

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159 <213> ORGANISM: homo sapiens
161 <400> SEQUENCE: 3
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163 cgtgtgacca gtgaagttct cacttgcat aagctgatta aaatgtacac atgggagaaa 120
164 ccatttgcaa aaatcattga agacctaaaga aggaaggaaa ggaagctatt ggagaagtgc 180
165 gggcttgctc agagcctgac aagtataacc ttgttcatca tccccacagt ggccacagcg 240
166 gtctgggttc tcatccacac atccttaaaag ctgaaactca cagcgtcaat ggccttcagc 300
167 atgctggcct ccttgaatct ccttcggctg tcagtgttct ttgtgcctat tgcagtcaaa 360
168 ggtctcacga attccaagtc tgcagtgatg aggttcaaga agtttttcct ccaggagagc 420
169 cctgttttct atgtccagac attacaagac cccagcaaag ctctggctct tgaggaggcc 480
170 acctgtgcat ggcaacagac ctgtcccggg atcgtcaatg gggcactgga gctggagagg 540
171 aacgggcatg cttctgaggg gatgaccagg cctagagatg ccctcgggcc agaggaagaa 600
172 gggaacagcc tgggcccaga gttgcacaag atcaacctgg tgggtgtcaa ggggatgatg 660
173 ttaggggtct gcggcaacac ggggagtggt aagagcagcc tgttgtcagc catcctggag 720
174 gagatgact tgcctgaggg ctcggtgggg gtgcagggaa gcctggccta tgtccccag 780
175 caggcctgga tcgtcagcgg gaacatcagg gagaacatcc tcatgggagg cgcataatgac 840
176 aaggcccgat acctccaggt gctccactgc tgctccctga atcgggacct ggaacttctg 900
177 ccctttggag acatgacaga gattggagag cggggcctca acctctctgg ggggcagaaa 960
178 cagaggatca gcctggcccg cgccgtctat tccgaccgtc agatctacct gctggacgac 1020
179 cccctgtctg ctgtggacgc ccacgtgggg aagcacattt ttgaggagtg cattaagaag 1080
180 aactcaggg ggaagacggt cgtcctgggtg acccaccagc tgcagtactt agaattttgt 1140
181 ggccagatca ttttgttgga aaatgggaaa atctgtgaaa atggaactca cagtgaattt 1200
182 atgcagaaaa aggggaaata tgcccaactt atccagaaga tgcacaagga agccacttcg 1260
183 gacatgttgc aggacacagc aaagatagca gagaagccaa aggtagaaaag tcaggctctg 1320
184 gccacctccc tggaagagtc tctcaacgga aatgctgtgc cggagcatca gctcacacag 1380
185 gaggaggaga tggaagaagg ctcttgagt tggagggtct accaccata catccaggca 1440
186 gctggagggt acatggtctc ttgcataatt ttcttctctg tgggtgctgat cgtcttctta 1500
187 acgatcttca gcttctggtg gctgagctac tgggtggagc agggctcggg gaccaatagc 1560
188 agccgagaga gcaatggaac catggcagac ctgggcaaca ttgcagacaa tcctcaactg 1620
189 tccttctacc agctggtgta cgggctcaac gccctgctcc tcatctgtgt gggggtctgc 1680
190 tcctcagggg ttttcaccaa ggtcacgagg aaggcatcca cggccctgca caacaagctc 1740
191 ttcaacaagg ttttcgctg ccccatgagt ttctttgaca ccatcccaat aggccggctt 1800
192 ttgaactgct tcgcagggga cttggaacag ctggaccagc tcttgcccat cttttcagag 1860
193 cagttcctgg tcctgtcctt aatggtgatc gccgtcctgt tgattgtcag tgtgctgtct 1920
194 ccatatatcc tgtaaatggg agccataatc atggttattt gcttcattta ttatatgatg 1980
195 ttcaagaagg ccatcgggtg gtcaagaga ctggagaact atagccggtc tcctttattc 2040
196 tcccatatcc tcaattctct gcaaggcctg agtccatcc atgtctatgg aaaaactgaa 2100
197 gacttcatca gccag 2115
199 <210> SEQ ID NO: 4
200 <211> LENGTH: 705
201 <212> TYPE: PRT
202 <213> ORGANISM: homo sapiens
204 <400> SEQUENCE: 4
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206 1 5 10 15
207 Asp Gln Arg Ile Arg Val Thr Ser Glu Val Leu Thr Cys Ile Lys Leu
208 20 25 30
209 Ile Lys Met Tyr Thr Trp Glu Lys Pro Phe Ala Lys Ile Ile Glu Asp
210 35 40 45

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211	Leu	Arg	Arg	Lys	Glu	Arg	Lys	Leu	Leu	Glu	Lys	Cys	Gly	Leu	Val	Gln
212		50					55					60				
213	Ser	Leu	Thr	Ser	Ile	Thr	Leu	Phe	Ile	Ile	Pro	Thr	Val	Ala	Thr	Ala
214	65				70						75					80
215	Val	Trp	Val	Leu	Ile	His	Thr	Ser	Leu	Lys	Leu	Lys	Leu	Thr	Ala	Ser
216				85						90					95	
217	Met	Ala	Phe	Ser	Met	Leu	Ala	Ser	Leu	Asn	Leu	Leu	Arg	Leu	Ser	Val
218				100					105					110		
219	Phe	Phe	Val	Pro	Ile	Ala	Val	Lys	Gly	Leu	Thr	Asn	Ser	Lys	Ser	Ala
220			115					120					125			
221	Val	Met	Arg	Phe	Lys	Lys	Phe	Phe	Leu	Gln	Glu	Ser	Pro	Val	Phe	Tyr
222		130					135					140				
223	Val	Gln	Thr	Leu	Gln	Asp	Pro	Ser	Lys	Ala	Leu	Val	Phe	Glu	Glu	Ala
224	145				150						155					160
225	Thr	Leu	Ser	Trp	Gln	Gln	Thr	Cys	Pro	Gly	Ile	Val	Asn	Gly	Ala	Leu
226				165						170					175	
227	Glu	Leu	Glu	Arg	Asn	Gly	His	Ala	Ser	Glu	Gly	Met	Thr	Arg	Pro	Arg
228				180					185					190		
229	Asp	Ala	Leu	Gly	Pro	Glu	Glu	Glu	Gly	Asn	Ser	Leu	Gly	Pro	Glu	Leu
230			195					200					205			
231	His	Lys	Ile	Asn	Leu	Val	Val	Ser	Lys	Gly	Met	Met	Leu	Gly	Val	Cys
232		210					215					220				
233	Gly	Asn	Thr	Gly	Ser	Gly	Lys	Ser	Ser	Leu	Leu	Ser	Ala	Ile	Leu	Glu
234	225				230						235					240
235	Glu	Met	His	Leu	Leu	Glu	Gly	Ser	Val	Gly	Val	Gln	Gly	Ser	Leu	Ala
236				245						250					255	
237	Tyr	Val	Pro	Gln	Gln	Ala	Trp	Ile	Val	Ser	Gly	Asn	Ile	Arg	Glu	Asn
238				260					265					270		
239	Ile	Leu	Met	Gly	Gly	Ala	Tyr	Asp	Lys	Ala	Arg	Tyr	Leu	Gln	Val	Leu
240			275					280					285			
241	His	Cys	Cys	Ser	Leu	Asn	Arg	Asp	Leu	Glu	Leu	Leu	Pro	Phe	Gly	Asp
242		290					295					300				
243	Met	Thr	Glu	Ile	Gly	Glu	Arg	Gly	Leu	Asn	Leu	Ser	Gly	Gly	Gln	Lys
244	305				310						315					320
245	Gln	Arg	Ile	Ser	Leu	Ala	Arg	Ala	Val	Tyr	Ser	Asp	Arg	Gln	Ile	Tyr
246				325						330					335	
247	Leu	Leu	Asp	Asp	Pro	Leu	Ser	Ala	Val	Asp	Ala	His	Val	Gly	Lys	His
248				340					345					350		
249	Ile	Phe	Glu	Glu	Cys	Ile	Lys	Lys	Thr	Leu	Arg	Gly	Lys	Thr	Val	Val
250			355					360					365			
251	Leu	Val	Thr	His	Gln	Leu	Gln	Tyr	Leu	Glu	Phe	Cys	Gly	Gln	Ile	Ile
252		370					375					380				
253	Leu	Leu	Glu	Asn	Gly	Lys	Ile	Cys	Glu	Asn	Gly	Thr	His	Ser	Glu	Leu
254	385				390						395					400
255	Met	Gln	Lys	Lys	Gly	Lys	Tyr	Ala	Gln	Leu	Ile	Gln	Lys	Met	His	Lys
256				405						410					415	
257	Glu	Ala	Thr	Ser	Asp	Met	Leu	Gln	Asp	Thr	Ala	Lys	Ile	Ala	Glu	Lys
258				420					425					430		
259	Pro	Lys	Val	Glu	Ser	Gln	Ala	Leu	Ala	Thr	Ser	Leu	Glu	Glu	Ser	Leu

VERIFICATION SUMMARY

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L:18 M:270 C: Current Application Number differs, Replaced Current Application No

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date